DETAILED ACTION

Continued Examination Under 37 CFR 1.114

A request for continued examination under 37 CFR 1.114, including the fee set

forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this

application is eligible for continued examination under 37 CFR 1.114, and the fee set

forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action

has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on

2/26/2010 has been entered.

Status of Claims

Claims 2 and 14 are cancelled. Claims 1, 3-13, 15 and 16 are currently pending

and examined on the merits.

Withdrawn Rejections/Objections

Rejections and/or objections not reiterated from previous office actions are

hereby withdrawn because of the amendments filed 2/26/2010. The following rejections

and/or objections are either reiterated or newly applied. They constitute the complete

set presently being applied to the instant application.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of
matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the
conditions and requirements of this title.

Claims 1, 3-13, 15 and 16 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter.

The recent en banc decision regarding Bilski v. Warsaw (2008) set forth that a process is patent-eligible if (1) it is tied to a particular machine or apparatus or (2) it transforms a particular article into a different state or thing.

The instant claims are drawn to a method for visualizing correlation data concerning two biological events or correlation and feature data in a matrix format as well as a general computer program product containing a program to said method. The instant claims are drawn to the abstract process steps of acquiring correlation and feature data, processing the correlation and feature data, and displaying the correlation and feature data.

The instant claims do not recite or inherently involve any transformation of an article, or recite any limitation that ties the recited abstract process to any particular machine or apparatus. Reciting that a method is performed by a suitably programmed computer in the preamble does not TIE a specific step of the method to a particular machine or apparatus. A specific step of the method must be tied to a particular machine or apparatus.

Nominal or token recitations will not suffice, E.g. displaying, inputting, obtaining, See Ex parte Langemyr (May 28, 2008). These recitations are considered insignificant extra-solution activities and will not meet the "transformation of an article" test. Applicants are cautioned against introduction of new matter in an amendment.

Claims 15 and 16 are drawn to a computer readable medium comprising

instructions for visualizing correlation data. The instant specification does not explicitly

define the scope of the limitation of "computer readable medium." The computer

program product/computer readable media is not limited to a physical embodiment and

may read on carrier waves and other nonstatutory media. See, e.g., In re Nuitjen,

Docket no. 2006-1371 (Fed. Cir. Sept. 20, 2007)(slip. op. at 18)("A transitory,

propagating signal like Nuitjen's is not a process, machine, manufacture, or composition

of matter.' … Thus, such a signal cannot be patentable subject matter.").

For these reasons, claims 1, 3-13, 15 and 16 are considered non-statutory

subject matter.

Response to Arguments

Applicant's arguments filed 2/26/2010 have been fully considered but they are

not persuasive.

Applicants argue that that the instant claims meet both prongs of the machine-or-

transformation test because the method is performed "in a suitably programmed

computer" and claim 15 is directed to a computer-readable programmable recording

medium in with a program….is stored, thus meeting the tied to a particular machine

prong of the test. Applicants argue that the tangible visual depiction of a relationship

between biological events in instant claims is like the transformation of Abele and thus

suffices from the transformation of a particular article prong. Applicants argue the

instant claims do not pre-empt a natural phenomenon.

Applicant's arguments are not persuasive. The instant method claims 1, 3-13,

are merely abstract process steps that do not have a tie of a particular step of the

method to a particular machine. Reciting that a method is performed by a suitably

programmed computer in the preamble does not tie any particular step of the method to

a particular machine or apparatus. A specific step of the method must be tied to a

particular machine or apparatus. The two prong analysis recited in *In re Bilski* is only

applicable to method claims, not to the computer product claims of 15 and 16. A

tangible visual depiction of a relationship of events is not a transformation of a particular

article or thing, as in Abele. There is no transformation of one type of data into a

different article or thing.

With regard to the computer readable medium, it is noted that a transitory signal

such as a carrier wave, or program, per se, is not considered statutory subject matter,

as set forth in In re Nuitjen (see above). The computer readable recording medium of

claims 15 and 16 are not limited to non-transitory embodiments, and thus encompass

signals. For these reasons, the rejection is maintained.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all

obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set
> forth in section 102 of this title, if the differences between the subject matter sought to be patented and
> the prior art are such that the subject matter as a whole would have been obvious at the time the

invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

The factual inquiries set forth in *Graham* **v.** *John Deere Co.,* 383 U.S. 1, 148 USPQ 459 (1966), that are applied for establishing a background for determining obviousness under 35 U.S.C. 103(a) are summarized as follows:

1.   Determining the scope and contents of the prior art.
2.   Ascertaining the differences between the prior art and the claims at issue.
3.   Resolving the level of ordinary skill in the pertinent art.
4.   Considering objective evidence present in the application indicating obviousness or nonobviousness.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claims 1, 3-10, 12, 13, 15 and 16 are rejected under 35 U.S.C. 103(a) as being unpatentable over Ge et al. (Nature Genetics, 2001, 29, 482-486) in view of Cras et al. (US 2002/0091681).

The instant claims provide a method for visualizing correlation data concerning two biological events, or the correlation data and feature data regarding each event, in a matrix format, the method comprising acquiring and processing correlation and feature data, displaying correlation data concerning biological events of the same or different

kinds, or the correlation data and feature data regarding each biological event in (a) one

of a plurality of prepared data display formats and at (b) one of a plurality of prepared

summarization levels, both of which are selected either manually or automatically

depending on the number of data items in desired display data, to visualize the

correlation and feature data.

Regarding claims 1 and 9, Ge et al. acquired protein-protein pair (feature data)

and corresponding genes (correlation data) from three experiments, (page 485, right

column, second paragraph) and processed the correlation and feature data, (page 485,

right column, last paragraph – page 486). Ge et al. shows a transcriptome-interactome

correlation mapping strategy of displaying pair-wise combinations between the clusters

of an expression profiling experiment, with numbers assigned to each cluster in rows

and columns of the matrix along with the number of genes each cluster contains in

parenthesis, wherein the table on the right shows protein interaction pairs together

(feature data) with the expression cluster to which the corresponding genes belong

(correlation data), wherein these expression clusters and corresponding genes are

displayed simultaneously, (page 482, right column, last paragraph - page 483, left

column, first paragraph; Figure 1). Ge et al. shows a table of an interaction pair (A), a

table of clusters of an expression profiling experiment (B), and a table showing the

probability for obtaining at least k observed groups in the intracluster region by chance

(C) (Figure 1; Table 1).

Ge et al. does not show summarization levels.

Cras et al. shows a system and method for creating an analytical report on top of

a multidimensional data model built on top of a relational or multidimensional database,

wherein, based on rules or queries, a summarization of levels of data may be supplied,

(paragraphs 9-13, 48-70, 110-116, 120-121, 129, 174).

Regarding claim 3, Ge et al. shows a two-dimensional matrix by organizing

clusters derived from a set of related transcriptional profiling experiments into tow

identical axes, wherein pairs of genes whose product can interact, according to the

clusters to which each gene belongs, (correlation info); For each square, an index of

protein interaction density (PID) as the ratio of the number of observed protein

interaction pairs to the total number of possible pair-wise combination of protein pairs is

calculated (attribute information), (page 483, left column, first paragraph).

Regarding claim 4, Ge et al. shows transcriptome-interactome correlation maps,

with calculated protein interaction density (PID) for each square in the matrix as the

ratio of interaction of pairs assigned to the square (IP) over the total number of protein

pairs possibly formed by combination of the genes in the square (PP) and running

diagonally from left to right and indicated by color, (Figure 2).

Regarding claim 5, Ge et al. shows data reduced to a character type (protein

interaction pairs) and numeric value type (numbers assigned to each cluster, number of

genes each cluster contains, (Figure 1).

Regarding claims 6 and 7, Ge et al. shows character type (protein interaction

pairs) and numeric value type (numbers assigned to each cluster, number of genes

each cluster contains in a layered structure, a keyword (ORF), rounding values to

significant digits and signs or colors indicating ORF pairs, (Figures 1-3, Table 1).

Regarding claim 8, Cras et al. shows a mechanisms which the results of a

multidimensional query are processed such that their format and contents accurately

reflect the semantics of an entity/relationship report specification, such that the tabular

and cross-tabulated reports may be executed using an online analytical programming

query, (paragraphs 110-116).

Regarding claim 10, Ge et al. shows protein-protein interactions and clustering

analysis data sets of cell cycle-regulated genes, meiosis-regulated genes and cell

stress-regulated genes, (page 485, right column, second paragraph).

Regarding claims 12 and 13, Ge et al. shows that a feature quantity common to

members of the cluster are the proteins produced by the genes of the cluster, interact

with one another, (abstract, Figure 1). Ge et al. shows a plurality of genes that encode

a plurality of interacting proteins wherein these PIDs are expressed in color, (Figures 2-

3).

Regarding claim 15, Ge et al. provides a k-means algorithm for clustering

analysis with the yeast cell-cycle expression data, (page 483, left column, last

paragraph).

Cras et al. shows a computer readable medium having computer readable code

embodied for use in the execution of a method of transforming results of a query into

results of a report, (paragraph 108, claim 13).

Regarding claim 16, Ge et al. acquired protein-protein pair (feature data) and

corresponding genes (correlation data) from three experiments, (page 485, right

column, second paragraph) and processed the correlation and feature data, (page 485,

right column, last paragraph – page 486). Ge et al. shows a transcriptome-interactome

correlation mapping strategy of displaying pair-wise combinations between the clusters

of an expression profiling experiment, with numbers assigned to each cluster in rows

and columns of the matrix along with the number of genes each cluster contains in

parenthesis, wherein the table on the right shows protein interaction pairs together

(feature data) with the expression cluster to which the corresponding genes belong

(correlation data), wherein these expression clusters and corresponding genes are

displayed simultaneously, (page 482, right column, last paragraph - page 483, left

column, first paragraph; Figure 1). Ge et al. shows a table of an interaction pair (A), a

table of clusters of an expression profiling experiment (B), and a table showing the

probability for obtaining at least k observed groups in the intracluster region by chance

(C) (Figure 1; Table 1). Ge et al. shows that a feature quantity common to members of

the cluster are the proteins produced by the genes of the cluster, interact with one

another, (abstract, Figure 1). Ge et al. shows a plurality of genes that encode a plurality

of interacting proteins wherein these PIDs are expressed in color, (Figures 2-3).

Cras et al. shows a system and method for creating an analytical report on top of

a multidimensional data model built on top of a relational or multidimensional database,

wherein based on rules or queries a summarization of levels of data may be supplied,

(paragraphs 9-13, 48-70, 110-116, 120-121, 129, 174). Cras et al. shows a computer

readable medium having computer readable code embodied for use in the execution of

a method of transforming results of a query into results of a report, (paragraph 108,

claim 13).

It would have been obvious to one of ordinary skill in the art at the time of the

instant invention to modify the transcriptome-interactome correlation mapping method

by Ge et al. with the summarization levels of Cras et al. because Cras et al. shows the

importance of clustering (grouping) data based on attributes into a hierarchy of levels

and aggregating fact values at different levels of summarization, and a person of

ordinary skill in the art would understand that visualizing data with the aid of levels of

summarization would enable better visualization of the correlation of data, (Cras et al.,

paragraph 172-176). Likewise, it would be obvious that protein-protein interactions

encompass protein-peptide interactions wherein peptides encompass compounds of

low molecular weight. Therefore, one of ordinary skill in the art would recognize the

claimed process as a combination of routine applications that are well known the art that

and produce no more than expected results.

Response to Arguments

Applicant's arguments filed 2/26/2010 have been fully considered but they are

not persuasive.

Applicants argue that the "events" of claim 1, are "biological events", not the

trascriptome-interactome analysis and gene interactions of Ge et al. Applicants argue

that Ge et al. does not disclose the plurality of display formats of claim 1.   Applicants

argue that Table 1 is not incorporated into a plurality of display formats which displays

correlation data in a matrix format. Cras et al. and Artymiuk do not remedy these

deficiencies.

Applicants arguments are not persuasive.

Ge et al. teaches the limitation of "acquiring correlation data concerning

biological events", i.e. protein-protein pair (feature data) and corresponding genes

(correlation data) from three experiments, (page 485, right column, second paragraph).

Ge et al. shows a plurality of display formats, e.g. 2D and 3D expression cluster

matrices, interaction pair table and interaction triplet table in a matrix formats, (See

Figure 1). Cras et al. shows a plurality of prepared summarization levels, as required by

the instant claims, (e.g. paragraphs 11, 12, 48-70). For these reasons, the examiner

maintains that the combination of teachings of the prior art renders the claimed

limitations obvious.

Claims 1, 3-13, 15 and 16 are rejected under 35 U.S.C. 103(a) as being

unpatentable over Ge et al. (Nature Genetics, 2001, 29, 482-486) in view of Cras et al.

(US 2002/0091681) as applied to claims 1, 3-10, 12, 13, 15 and 16 above, and further in

view of Artymiuk et al. (J. Mol. Biol., 1994, 243, 327-344).

The instant claim 11 depends from claim 1 with the extra limitation that

as the biological events, a structural unit is defined on the basis of atoms in a molecule

or a set of atoms in a molecule for each molecule in a complex of one or more

molecules, a representative position of the structural unit is defined on the basis of the

coordinates of atoms of which the structural unit is composed, and information about the distance between the representative positions of the structural units is displayed in the cells in the matrix, said matrix having each of the structural units as elements in the rows and columns thereof.

Ge et al. and Cras et al. are applied to claims 1, 3-10, 12, 13, 15 and 16 above.

Regarding claim 11, Ge et al. and Cras et al. do not show a matrix with rows and columns of cells encompassing structural units of molecules, wherein the structural unit are atom(s) in a molecule, with information about distances between structural units.

Artymiuk et al. shows a matrix with rows and columns of cells encompassing structural units of a protein, wherein the structural units are the atoms of amino acids (Histidine 57, Serine 195 and Aspartate 102) encompassing a serine-protease catalytic triad, and providing distances between the respective structural units, (page 331; Figures 2-3).

It would have been obvious to one of ordinary skill in the art at the time of the instant invention to modify the transcriptome-interactome correlation mapping method by Ge et al. with the summarization levels of Cras et al. and the search matrix of structural units with respective distances by Artymiuk et al. because a search matrix is a subgraph that is searched for in graphs that contains the necessary parts as required for a particular search pattern (structural units) and allows one skilled in the art to minimize the storage overhead and greatly reduce the input-output overheads that would be involved in reading large pre-calculated matrices, (Artymiuk, page 331, right column, penultimate paragraph).

Response to Arguments

Applicant's arguments filed 2/26/2010 have been fully considered but they are not persuasive.

Applicants argue that Ge, Cras and Artymiuk do not disclose the limitations of the amended claims.

Applicants arguments are not persuasive for the same reasons as those set forth above.

Conclusion

No claims are allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to LARRY D. RIGGS II whose telephone number is (571)270-3062. The examiner can normally be reached on Monday-Thursday, 7:30AM-5:00PM, ALT. Friday, EST.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Marjorie Moran can be reached on 571-272-0720. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the

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system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

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